

SEQUENCE LISTING

<110> Curtis, Rory A.J.

<120> 52906, 33408, AND 12189, NOVEL POTASSIUM
CHANNEL FAMILY MEMBERS AND USES THEREOF

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<150> US 60/209,845

<151> 2000-06-06

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Asn Tyr Glu Ser Asn Cys Phe Glu Val Leu Leu Tyr Lys Lys Asn Arg	90	95	100	
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Thr Pro Val Trp Phe Tyr Met Gln Ile Ala Pro Ile Arg Asn Glu His	105	110	115	
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Glu Lys Val Val Leu Phe Leu Cys Thr Phe Lys Asp Ile Thr Leu Phe	120	125	130	
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Ala Pro Lys Thr Pro Pro His Ile Ile Leu His Tyr Cys Ala Phe Lys	200	205	210	
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Val Leu Asn Phe His Thr Thr Phe Val Gly Pro Gly Gly Glu Val Ile	265	270	275	
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Ser Asp Pro Lys Leu Ile Arg Met Asn Tyr Leu Lys Thr Trp Phe Val	280	285	290	

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 Cys Ser Phe Met Tyr Gly Glu Leu Thr Asp Lys Lys Thr Ile Glu Lys
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gcccgaagtc cgctagagca cagtcccatc caggctgatg ccaagcacc cttttatccc 2700
atccccgagc aggccttaca gaccacactg caggaagtca aacacgaact caaagaggac 2760
atccagctgc tcagctgcag aatgactgcc ctagaaaagc aggtggcaga aattttaaaa 2820
atactgtcgg aaaaaagcgt accccaggcc tcatctccca aatoccaa atgccactcaa 2880
gtaccccccc agataccatg tcaggatatt tttagtgtct caaggcctga atcacctgaa 2940
tctgacaaag atgaaatcca ctttttaa 2967

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<211> 1341

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1338)

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Cys Cys Glu Arg Leu Val Leu Asn Val Ala Gly Leu Arg Phe Glu Thr
1 5 10 15

cgg gcg cgc acg ctg ggc cgc ttc ccg gac act ctg cta ggg gac cca 96
Arg Ala Arg Thr Leu Gly Arg Phe Pro Asp Thr Leu Leu Gly Asp Pro
20 25 30

gcg cgc cgc ggc cgc ttc tac gac gac gcg cgc cgc gag tat ttc ttc 144
Ala Arg Arg Gly Arg Phe Tyr Asp Asp Ala Arg Arg Glu Tyr Phe Phe
35 40 45

gac cgg cac cgg ccc agc ttc gac gcc gtg ctc tac tac tac cag tcc 192
Asp Arg His Arg Pro Ser Phe Asp Ala Val Leu Tyr Tyr Tyr Gln Ser
50 55 60

ggg ggg cgg ctg cgg cgg ccg gcg cac gtg ccg ctc gac gtc ttc ctg 240
Gly Gly Arg Leu Arg Arg Pro Ala His Val Pro Leu Asp Val Phe Leu

65	70	75	80	
gaa gag gtg gcc ttc tac ggg ctg ggc gcg gcg gcc ctg gca cgc ctg				288
Glu Glu Val Ala Phe Tyr Gly Leu Gly Ala Ala Ala Leu Ala Arg Leu	85	90	95	
cgc gag gac gag ggc tgc ccg gtg ccg ccc gag cgc ccc ctg ccc cgc				336
Arg Glu Asp Glu Gly Cys Pro Val Pro Pro Glu Arg Pro Leu Pro Arg	100	105	110	
cgc gcc ttc gcc cgc cag ctg tgc ctg ctt ttc gag ttt ccc gag agc				384
Arg Ala Phe Ala Arg Gln Leu Cys Leu Leu Phe Glu Phe Pro Glu Ser	115	120	125	
tct cag gcc gcg cgc gtg ctc gcc gta gtc tcc gtg ctg gtc atc ctc				432
Ser Gln Ala Ala Arg Val Leu Ala Val Val Ser Val Leu Val Ile Leu	130	135	140	
gtc tcc atc gtc gtc ttc tgc ctc gag acg ctg cct gac ttc cgc gac				480
Val Ser Ile Val Val Phe Cys Leu Glu Thr Leu Pro Asp Phe Arg Asp	145	150	155	160
gac cgc gac ggc acg ggg ctt gct gct gca gcc gca gcc ggc ccg ttc				528
Asp Arg Asp Gly Thr Gly Leu Ala Ala Ala Ala Ala Gly Pro Phe	165	170	175	
ccc gct ccg ctg aat ggc tcc agc caa atg cct gga aat cca ccc cgc				576
Pro Ala Pro Leu Asn Gly Ser Ser Gln Met Pro Gly Asn Pro Pro Arg	180	185	190	
ctg ccc ttc aat gac ccg ttc ttc gtg gtg gag acg ctg tgt att tgt				624
Leu Pro Phe Asn Asp Pro Phe Phe Val Val Glu Thr Leu Cys Ile Cys	195	200	205	
tgg ttc tcc ttt gag ctg ctg gta cgc ctc ctg gtc tgt cca agc aag				672
Trp Phe Ser Phe Glu Leu Leu Val Arg Leu Leu Val Cys Pro Ser Lys	210	215	220	
gct atc ttc ttc aag aac gtg atg aac ctc atc gat ttt gtg gct atc				720
Ala Ile Phe Phe Lys Asn Val Met Asn Leu Ile Asp Phe Val Ala Ile	225	230	235	240
ctt ccc tac ttt gtg gca ctg ggc acc gag ctg gcc cgg cag cga ggg				768
Leu Pro Tyr Phe Val Ala Leu Gly Thr Glu Leu Ala Arg Gln Arg Gly	245	250	255	
gtg ggc cag cag gcc atg tca ctg gcc atc ctg aga gtc atc cga ttg				816
Val Gly Gln Gln Ala Met Ser Leu Ala Ile Leu Arg Val Ile Arg Leu	260	265	270	
gtg cgt gtc ttc cgc atc ttc aag ctg tcc cgg cac tca aag ggc ctg				864
Val Arg Val Phe Arg Ile Phe Lys Leu Ser Arg His Ser Lys Gly Leu	275	280	285	
caa atc ttg ggc cag acg ctt cgg gcc tcc atg cgt gag ctg ggc ctc				912
Gln Ile Leu Gly Gln Thr Leu Arg Ala Ser Met Arg Glu Leu Gly Leu	290	295	300	

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<400> 8																
Cys	Cys	Glu	Arg	Leu	Val	Leu	Asn	Val	Ala	Gly	Leu	Arg	Phe	Glu	Thr	
1				5					10					15		
Arg	Ala	Arg	Thr	Leu	Gly	Arg	Phe	Pro	Asp	Thr	Leu	Leu	Gly	Asp	Pro	
			20					25					30			
Ala	Arg	Arg	Gly	Arg	Phe	Tyr	Asp	Asp	Ala	Arg	Arg	Glu	Tyr	Phe	Phe	
		35					40					45				
Asp	Arg	His	Arg	Pro	Ser	Phe	Asp	Ala	Val	Leu	Tyr	Tyr	Tyr	Gln	Ser	
	50					55					60					
Gly	Gly	Arg	Leu	Arg	Arg	Pro	Ala	His	Val	Pro	Leu	Asp	Val	Phe	Leu	
65					70					75					80	
Glu	Glu	Val	Ala	Phe	Tyr	Gly	Leu	Gly	Ala	Ala	Ala	Leu	Ala	Arg	Leu	
				85					90					95		

Arg Glu Asp Glu Gly Cys Pro Val Pro Pro Glu Arg Pro Leu Pro Arg
 100 105 110
 Arg Ala Phe Ala Arg Gln Leu Cys Leu Leu Phe Glu Phe Pro Glu Ser
 115 120 125
 Ser Gln Ala Ala Arg Val Leu Ala Val Val Ser Val Leu Val Ile Leu
 130 135 140
 Val Ser Ile Val Val Phe Cys Leu Glu Thr Leu Pro Asp Phe Arg Asp
 145 150 155 160
 Asp Arg Asp Gly Thr Gly Leu Ala Ala Ala Ala Ala Gly Pro Phe
 165 170 175
 Pro Ala Pro Leu Asn Gly Ser Ser Gln Met Pro Gly Asn Pro Pro Arg
 180 185 190
 Leu Pro Phe Asn Asp Pro Phe Phe Val Val Glu Thr Leu Cys Ile Cys
 195 200 205
 Trp Phe Ser Phe Glu Leu Leu Val Arg Leu Leu Val Cys Pro Ser Lys
 210 215 220
 Ala Ile Phe Phe Lys Asn Val Met Asn Leu Ile Asp Phe Val Ala Ile
 225 230 235 240
 Leu Pro Tyr Phe Val Ala Leu Gly Thr Glu Leu Ala Arg Gln Arg Gly
 245 250 255
 Val Gly Gln Gln Ala Met Ser Leu Ala Ile Leu Arg Val Ile Arg Leu
 260 265 270
 Val Arg Val Phe Arg Ile Phe Lys Leu Ser Arg His Ser Lys Gly Leu
 275 280 285
 Gln Ile Leu Gly Gln Thr Leu Arg Ala Ser Met Arg Glu Leu Gly Leu
 290 295 300
 Leu Ile Phe Phe Leu Phe Ile Gly Val Val Leu Phe Ser Ser Ala Val
 305 310 315 320
 Tyr Phe Ala Glu Val Asp Arg Val Asp Ser His Phe Thr Ser Ile Pro
 325 330 335
 Glu Ser Phe Trp Trp Ala Val Val Thr Met Thr Thr Val Gly Tyr Gly
 340 345 350
 Asp Met Ala Pro Val Thr Val Gly Gly Lys Ile Val Gly Ser Leu Cys
 355 360 365
 Ala Ile Ala Gly Val Leu Thr Ile Ser Leu Pro Val Pro Val Ile Val
 370 375 380
 Ser Asn Phe Ser Tyr Phe Tyr His Arg Glu Thr Glu Gly Glu Glu Ala
 385 390 395 400
 Gly Met Phe Ser His Val Asp Met Gln Pro Cys Gly Pro Leu Glu Gly
 405 410 415
 Lys Ala Asn Gly Gly Leu Val Asp Gly Glu Val Pro Glu Leu Pro Pro
 420 425 430
 Pro Leu Trp Ala Pro Pro Gly Lys His Leu Val Thr Glu Val
 435 440 445

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 <211> 223
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<400> 9
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 1 5 10 15
 Ile Val Leu Lys Phe Ile Ala Tyr Gly Leu Lys Ser Thr Ser Asn Ile

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      20              25              30
Ala Ala Lys Tyr Leu Lys Ser Ile Phe Asn Ile Leu Asp Leu Leu Ala
      35              40              45
Ile Leu Pro Leu Leu Leu Leu Leu Val Leu Phe Leu Ser Gly Thr Glu
      50              55              60
Gln Val Ala Lys Lys Arg Leu Arg Glu Arg Phe Ser Leu Glu Leu Ser
65      70      75      80
Gln Trp Tyr Tyr Arg Ile Leu Arg Phe Leu Arg Leu Leu Arg Leu Leu
      85      90      95
Arg Leu Leu Arg Leu Leu Arg Leu Leu Arg Arg Leu Glu Thr Leu Phe
      100      105      110
Glu Phe Glu Leu Gly Thr Leu Ala Trp Ser Leu Gln Ser Leu Gly Arg
      115      120      125
Ala Leu Lys Ser Ile Leu Arg Phe Leu Leu Leu Leu Leu Leu Leu
      130      135      140
Ile Gly Phe Ser Val Ile Gly Tyr Leu Leu Phe Lys Gly Tyr Glu Asp
145      150      155      160
Leu Ser Glu Asn Glu Val Asp Gly Asn Ser Glu Phe Ser Ser Tyr Phe
      165      170      175
Asp Ala Phe Tyr Phe Leu Phe Val Thr Leu Thr Thr Val Gly Phe Gly
      180      185      190
Asp Leu Val Pro Val Trp Leu Gly Ile Ile Phe Phe Val Leu Phe Phe
      195      200      205
Ile Ile Val Gly Leu Leu Leu Leu Asn Leu Leu Ile Ala Val Ile
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<210> 10

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<400> 10

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Gly Asp Pro Gly Asp Ser Phe Tyr Ile Val Leu Ser Gly Glu Val Glu
      20      25      30
Val Tyr Lys Leu Thr Glu Asp Gly Ala Arg Thr Pro Glu Val Ser Gln
      35      40      45
Lys Gln Asp Thr Arg Glu Gln Val Val Ala Thr Leu Gly Pro Gly Asp
50      55      60
Phe Phe Gly Glu Leu Ala Leu Leu Thr Asn Asp Gly Asn Lys Asn Ala
65      70      75      80
Val Leu Pro Ser Leu Asp Gln Gly Ala Pro Arg Thr Ala Thr Val Arg
      85      90      95
Ala Leu Thr Asp Ser Glu Leu Leu Arg Leu Asp Arg Glu Asp Phe Arg
      100      105      110
Arg Leu Leu Gln Lys Tyr Pro Glu
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<210> 11

<211> 111

<212> PRT

<213> Artificial Sequence

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<220>

<223> consensus sequence

<400> 11

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Ser	Thr	Leu	Thr	Arg	Phe	Lys	Pro	Asp	Thr	Leu	Leu	Gly	Arg	Leu	Leu
			20					25					30		
Lys	Thr	Asp	Ser	Asp	Val	His	Glu	Ala	Arg	Leu	Arg	Leu	Cys	Asp	Phe
		35					40					45			
Tyr	Asp	Asp	Glu	Thr	Gly	Glu	Tyr	Phe	Phe	Asp	Arg	Ser	Pro	Lys	His
	50					55					60				
Phe	Glu	Thr	Ile	Leu	Asn	Phe	Tyr	Arg	Thr	Gly	Asp	Gly	Lys	Leu	His
65					70					75					80
Arg	Pro	Glu	Val	Cys	Leu	Asp	Ser	Phe	Leu	Glu	Glu	Leu	Glu	Phe	Tyr
				85					90					95	
Gly	Leu	Asp	Glu	Leu	Ala	Ile	Glu	Ser	Cys	Cys	Glu	Asp	Glu	Tyr	
			100					105					110		

<210> 12

<211> 988

<212> PRT

<213> Rattus norvegicus

<400> 12

Met	Pro	Gly	Gly	Lys	Arg	Gly	Leu	Val	Ala	Pro	Gln	Asn	Thr	Phe	Leu
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Glu	Asn	Ile	Val	Arg	Arg	Ser	Ser	Glu	Ser	Ser	Phe	Leu	Leu	Gly	Asn
			20					25					30		
Ala	Gln	Ile	Val	Asp	Trp	Pro	Val	Val	Tyr	Ser	Asn	Asp	Gly	Phe	Cys
		35					40					45			
Lys	Leu	Ser	Gly	Tyr	His	Arg	Ala	Asp	Val	Met	Gln	Lys	Ser	Ser	Thr
	50					55					60				
Cys	Ser	Phe	Met	Tyr	Gly	Glu	Leu	Thr	Asp	Lys	Lys	Thr	Ile	Glu	Lys
65					70					75					80
Val	Arg	Gln	Thr	Phe	Asp	Asn	Tyr	Glu	Ser	Asn	Cys	Phe	Glu	Val	Leu
				85				90					95		
Leu	Tyr	Lys	Lys	Asn	Arg	Thr	Pro	Val	Trp	Phe	Tyr	Met	Gln	Ile	Ala
			100				105						110		
Pro	Ile	Arg	Asn	Glu	His	Glu	Lys	Val	Val	Leu	Phe	Leu	Cys	Thr	Phe
	115					120						125			
Lys	Asp	Ile	Thr	Leu	Phe	Lys	Gln	Pro	Ile	Glu	Asp	Asp	Ser	Thr	Lys
	130					135					140				
Gly	Trp	Thr	Lys	Phe	Ala	Arg	Leu	Thr	Arg	Ala	Leu	Thr	Asn	Ser	Arg
145					150					155					160
Ser	Val	Leu	Gln	Gln	Leu	Thr	Pro	Met	Asn	Lys	Thr	Glu	Thr	Val	His
				165					170					175	
Lys	His	Ser	Arg	Leu	Ala	Glu	Val	Leu	Gln	Leu	Gly	Ser	Asp	Ile	Leu
			180					185					190		
Pro	Gln	Tyr	Lys	Gln	Glu	Ala	Pro	Lys	Thr	Pro	Pro	His	Ile	Ile	Leu
	195						200						205		
His	Tyr	Cys	Ala	Phe	Lys	Thr	Thr	Trp	Asp	Trp	Val	Ile	Leu	Ile	Leu
	210					215					220				
Thr	Phe	Tyr	Thr	Ala	Ile	Met	Val	Pro	Tyr	Asn	Val	Ser	Phe	Lys	Thr
225					230					235					240
Lys	Gln	Asn	Asn	Ile	Ala	Trp	Leu	Val	Leu	Asp	Ser	Val	Val	Asp	Val
				245					250					255	

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Ile Phe Leu Val Asp Ile Val Leu Asn Phe His Thr Thr Phe Val Gly
 260 265 270
 Pro Gly Gly Glu Val Ile Ser Asp Pro Lys Leu Ile Arg Met Asn Tyr
 275 280 285
 Leu Lys Thr Trp Phe Val Ile Asp Leu Leu Ser Cys Leu Pro Tyr Asp
 290 295 300
 Ile Ile Asn Ala Phe Glu Asn Val Asp Glu Gly Ile Ser Ser Leu Phe
 305 310 315 320
 Ser Ser Leu Lys Val Val Arg Leu Leu Arg Leu Gly Arg Val Ala Arg
 325 330 335
 Lys Leu Asp His Tyr Leu Glu Tyr Gly Ala Ala Val Leu Val Leu Leu
 340 345 350
 Val Cys Val Phe Gly Leu Val Ala His Trp Leu Ala Cys Ile Trp Tyr
 355 360 365
 Ser Ile Gly Asp Tyr Glu Val Ile Asp Glu Val Thr Asn Thr Ile Gln
 370 375 380
 Ile Asp Ser Trp Leu Tyr Gln Leu Ala Leu Ser Ile Arg Thr Pro Tyr
 385 390 395 400
 Arg Tyr Asn Thr Ser Ala Gly Ile Trp Glu Gly Gly Pro Ser Lys Asp
 405 410 415
 Ser Leu Tyr Val Ser Ser Leu Tyr Phe Thr Met Thr Ser Leu Thr Thr
 420 425 430
 Ile Gly Phe Gly Asn Ile Ala Pro Thr Thr Asp Val Glu Lys Met Phe
 435 440 445
 Ser Val Ala Met Met Met Val Gly Ser Leu Leu Tyr Ala Thr Ile Phe
 450 455 460
 Gly Asn Val Thr Thr Ile Phe Gln Gln Met Tyr Ala Asn Thr Asn Arg
 465 470 475 480
 Tyr His Glu Met Leu Asn Asn Val Arg Asp Phe Leu Lys Leu Tyr Gln
 485 490 495
 Val Pro Lys Gly Leu Ser Glu Arg Val Met Asp Tyr Ile Val Ser Thr
 500 505 510
 Trp Ser Met Ser Lys Gly Ile Asp Thr Glu Lys Val Leu Ser Ile Cys
 515 520 525
 Pro Lys Asp Met Arg Ala Asp Ile Cys Val His Leu Asn Arg Lys Val
 530 535 540
 Phe Asn Glu His Pro Ala Phe Arg Leu Ala Ser Asp Gly Cys Leu Arg
 545 550 555 560
 Ala Leu Ala Val Glu Phe Gln Thr Ile His Cys Ala Pro Gly Asp Leu
 565 570 575
 Ile Tyr His Ala Gly Glu Ser Val Asp Ala Leu Cys Phe Val Val Ser
 580 585 590
 Gly Ser Leu Glu Val Ile Gln Asp Glu Glu Val Val Ala Ile Leu Gly
 595 600 605
 Lys Gly Asp Val Phe Gly Asp Ile Phe Trp Lys Glu Thr Thr Leu Ala
 610 615 620
 His Ala Cys Ala Asn Val Arg Ala Leu Thr Tyr Cys Asp Leu His Ile
 625 630 635 640
 Ile Lys Arg Glu Ala Leu Leu Lys Val Leu Asp Phe Tyr Thr Ala Phe
 645 650 655
 Ala Asn Ser Phe Ser Arg Asn Leu Thr Leu Thr Cys Asn Leu Arg Lys
 660 665 670
 Arg Ile Ile Phe Arg Lys Ile Ser Asp Val Lys Lys Glu Glu Glu Glu
 675 680 685
 Arg Leu Arg Gln Lys Asn Glu Val Thr Leu Ser Ile Pro Val Asp His
 690 695 700
 Pro Val Arg Lys Leu Phe Gln Lys Phe Lys Gln Gln Lys Glu Leu Arg

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705 710 715 720
 Asn Gln Gly Ser Ala Gln Ser Asp Pro Glu Arg Ser Gln Leu Gln Val
 725 730 735
 Glu Ser Arg Pro Leu Gln Asn Gly Ala Ser Ile Thr Gly Thr Ser Val
 740 745 750
 Val Thr Val Ser Gln Ile Thr Pro Ile Gln Thr Ser Leu Ala Tyr Val
 755 760 765
 Lys Thr Ser Glu Thr Leu Lys Gln Asn Asn Arg Asp Ala Met Glu Leu
 770 775 780
 Lys Pro Asn Gly Gly Ala Glu Pro Lys Cys Leu Lys Val Asn Ser Pro
 785 790 795 800
 Ile Arg Met Lys Asn Gly Asn Gly Lys Gly Trp Leu Arg Leu Lys Asn
 805 810 815
 Asn Met Gly Ala His Glu Glu Lys Lys Glu Glu Trp Asn Asn Val Thr
 820 825 830
 Lys Ala Glu Ser Met Gly Leu Leu Ser Glu Asp Pro Lys Gly Ser Asp
 835 840 845
 Ser Glu Asn Ser Val Thr Lys Asn Pro Leu Arg Lys Thr Asp Ser Cys
 850 855 860
 Asp Ser Gly Ile Thr Lys Ser Asp Leu Arg Leu Asp Lys Ala Gly Glu
 865 870 875 880
 Ala Arg Ser Pro Leu Glu His Ser Pro Ser Gln Ala Asp Ala Lys His
 885 890 895
 Pro Phe Tyr Pro Ile Pro Glu Gln Ala Leu Gln Thr Thr Leu Gln Glu
 900 905 910
 Val Lys His Glu Leu Lys Glu Asp Ile Gln Leu Leu Ser Cys Arg Met
 915 920 925
 Thr Ala Leu Glu Lys Gln Val Ala Glu Ile Leu Lys Leu Leu Ser Glu
 930 935 940
 Lys Ser Val Pro Gln Thr Ser Ser Pro Lys Pro Gln Ile Pro Leu Gln
 945 950 955 960
 Val Pro Pro Gln Ile Pro Cys Gln Asp Ile Phe Ser Val Ser Arg Pro
 965 970 975
 Glu Ser Pro Glu Ser Asp Lys Asp Glu Ile Asn Phe
 980 985

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<211> 532

<212> PRT

<213> Mus musculus

<400> 13

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 Gly Val Thr Pro Pro Pro Pro Pro Arg Pro Gly Arg Thr Phe His Ala
 35 40 45
 Ile Phe Thr Arg Arg His Arg Thr Pro Asp Trp Gly Gly Cys Gly Val
 50 55 60
 Gly Ala Thr Arg Pro Phe Thr Gly Arg Pro Gly Cys Ala Arg His Gly
 65 70 75 80
 Ala Thr Val Pro Ala Ala Leu Arg Cys Cys Glu Arg Leu Val Leu Asn
 85 90 95
 Val Ala Gly Leu Arg Phe Glu Thr Arg Ala Arg Thr Leu Gly Arg Phe
 100 105 110
 Pro Asp Thr Leu Leu Gly Asp Pro Val Arg Arg Ser Arg Phe Tyr Asp

115 120 125
 Gly Ala Arg Ala Glu Tyr Phe Phe Asp Arg His Arg Pro Ser Phe Asp
 130 135 140
 Ala Val Leu Tyr Tyr Tyr Gln Ser Gly Gly Arg Leu Arg Arg Pro Ala
 145 150 155 160
 His Val Pro Leu Asp Val Phe Leu Glu Glu Val Ser Phe Tyr Gly Leu
 165 170 175
 Gly Arg Arg Leu Ala Arg Leu Arg Glu Asp Glu Gly Cys Ala Val Ala
 180 185 190
 Glu Arg Pro Leu Pro Pro Pro Phe Ala Arg Gln Leu Trp Leu Leu Phe
 195 200 205
 Glu Phe Pro Glu Ser Ser Gln Ala Ala Arg Val Leu Ala Val Val Ser
 210 215 220
 Val Leu Val Ile Leu Val Ser Ile Val Val Phe Cys Leu Glu Thr Leu
 225 230 235 240
 Pro Asp Phe Arg Asp Asp Arg Asp Asp Pro Gly Leu Ala Pro Val Ala
 245 250 255
 Ala Ala Thr Gly Ser Phe Leu Ala Arg Leu Asn Gly Ser Ser Pro Met
 260 265 270
 Pro Gly Ala Pro Pro Arg Gln Pro Phe Asn Asp Pro Phe Phe Val Val
 275 280 285
 Glu Thr Leu Cys Ile Cys Trp Phe Ser Phe Glu Leu Leu Val His Leu
 290 295 300
 Val Ala Cys Pro Ser Lys Ala Val Phe Phe Lys Asn Val Met Asn Leu
 305 310 315 320
 Ile Asp Phe Val Ala Ile Leu Pro Tyr Phe Val Ala Leu Gly Thr Glu
 325 330 335
 Leu Ala Arg Gln Arg Gly Val Gly Gln Pro Ala Met Ser Leu Ala Ile
 340 345 350
 Leu Arg Val Ile Arg Leu Val Arg Val Phe Arg Ile Phe Lys Leu Ser
 355 360 365
 Arg His Ser Lys Gly Leu Gln Ile Leu Gly Gln Thr Leu Arg Ala Ser
 370 375 380
 Met Arg Glu Leu Gly Leu Leu Ile Phe Phe Leu Phe Ile Gly Val Val
 385 390 395 400
 Leu Phe Ser Ser Ala Val Tyr Phe Ala Glu Val Asp Arg Val Asp Thr
 405 410 415
 His Phe Thr Ser Ile Pro Glu Ser Phe Trp Trp Ala Val Val Thr Met
 420 425 430
 Thr Thr Val Gly Tyr Gly Asp Met Ala Pro Val Thr Val Gly Gly Lys
 435 440 445
 Ile Val Gly Ser Leu Cys Ala Ile Ala Gly Val Leu Thr Ile Ser Leu
 450 455 460
 Pro Val Pro Val Ile Val Ser Asn Phe Ser Tyr Phe Tyr His Arg Glu
 465 470 475 480
 Thr Glu Gly Glu Glu Ala Gly Met Tyr Ser His Val Asp Thr Gln Pro
 485 490 495
 Cys Gly Thr Leu Glu Gly Lys Ala Asn Gly Gly Leu Val Asp Ser Glu
 500 505 510
 Val Pro Glu Leu Leu Pro Pro Leu Trp Pro Pro Ala Gly Lys His Met
 515 520 525
 Val Thr Glu Val
 530

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